



SEQUENCE LISTING

<110> Covacci, Antonello  
Bugnoli, Massimo  
Telford, John  
Macchia, Giovanni  
Rappuoli, Rino

<120> Helicobacter Pylori Cytotoxin Proteins Useful For  
Vaccines And Diagnostics

<130> CHIR0158

<140> 09/360,934

<141> 1999-07-26

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial  
Sequence

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial  
Sequence

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<211> 1296

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Sequence

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Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile  
35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly  
50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys  
65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys  
85 90 95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly  
100 105 110

Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln  
115 120 125

Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr  
 130 135 140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met  
 145 150 155 160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr  
 165 170 175

Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala  
 180 185 190

Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly  
 195 200 205

Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala  
 210 215 220

Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp  
 225 230 235 240

Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn  
 245 250 255

Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser  
 260 265 270

Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn  
 275 280 285

His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala  
 290 295 300

Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly  
 305 310 315 320

Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn  
 325 330 335

Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala  
 340 345 350

Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val  
 355 360 365

Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln  
 370 375 380

Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile  
 385 390 395 400

Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe  
 405 410 415

Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly  
 420 425 430

Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu  
 435 440 445

Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn  
 450 455 460

Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe  
 465 470 475 480

Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp  
 485 490 495

Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala  
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Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp  
 515 520 525

Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala  
 530 535 540

Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val  
 545 550 555 560

Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp  
 565 570 575

Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr  
 580 585 590

Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu  
 595 600 605

Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg  
 610 615 620

Asn Ile Lys Asn Val Glu Ile Thr Asn Lys Leu Ala Phe Gly Pro Gln  
 625 630 635 640

Gly	Ser	Pro	Trp	Gly	Thr	Ser	Lys	Leu	Met	Phe	Asn	Asn	Leu	Thr	Leu	645	650	655	
Gly	Gln	Asn	Ala	Val	Met	Asp	Tyr	Ser	Gln	Phe	Ser	Asn	Leu	Thr	Ile	660	665	670	
Gln	Gly	Asp	Phe	Ile	Asn	Asn	Gln	Gly	Thr	Ile	Asn	Tyr	Leu	Val	Arg	675	680	685	
Gly	Gly	Lys	Val	Ala	Thr	Leu	Ser	Val	Gly	Asn	Ala	Ala	Ala	Met	Met	690	695	700	
Phe	Asn	Asn	Asp	Ile	Asp	Ser	Ala	Thr	Gly	Phe	Tyr	Lys	Pro	Leu	Ile	705	710	715	720
Lys	Ile	Asn	Ser	Ala	Gln	Asp	Leu	Ile	Lys	Asn	Thr	Glu	His	Val	Leu	725	730	735	
Leu	Lys	Ala	Lys	Ile	Ile	Gly	Tyr	Gly	Asn	Val	Ser	Thr	Gly	Thr	Asn	740	745	750	
Gly	Ile	Ser	Asn	Val	Asn	Leu	Glu	Glu	Gln	Phe	Lys	Glu	Arg	Leu	Ala	755	760	765	
Leu	Tyr	Asn	Asn	Asn	Asn	Arg	Met	Asp	Thr	Cys	Val	Val	Arg	Asn	Thr	770	775	780	
Asp	Asp	Ile	Lys	Ala	Cys	Gly	Met	Ala	Ile	Gly	Asp	Gln	Ser	Met	Val	785	790	795	800
Asn	Asn	Pro	Asp	Asn	Tyr	Lys	Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Lys	Asn	805	810	815	
Ile	Gly	Ile	Ser	Lys	Thr	Ala	Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr	820	825	830	
Leu	Gly	Asn	Ser	Thr	Pro	Thr	Glu	Asn	Gly	Gly	Asn	Thr	Thr	Asn	Leu	835	840	845	
Pro	Thr	Asn	Thr	Thr	Ser	Asn	Ala	Arg	Ser	Ala	Asn	Asn	Ala	Leu	Ala	850	855	860	
Gln	Asn	Ala	Pro	Phe	Ala	Gln	Pro	Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala	865	870	875	880
Ile	Asn	Gln	His	Asp	Phe	Gly	Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	885	890	895	

Asn Arg Ser Lys Asp Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln		
900	905	910
Gly Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly		
915	920	925
Tyr Ala Arg Lys Met Ile Asp Ala Thr Ser Ala Asn Glu Ile Thr Lys		
930	935	940
Gln Leu Asn Thr Ala Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu		
945	950	955 960
His Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile		
	965 970	975
Leu Asn Ser Arg Leu Val Asn Leu Ser Arg Arg His Thr Asn His Ile		
	980 985	990
Asp Ser Phe Ala Lys Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala		
	995 1000	1005
Ser Leu Glu Ser Ala Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys Tyr		
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Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Thr Ser Leu		
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Asn Asn Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp		
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Ala Tyr Leu Asn Gly Gln Val Glu Ala Ile Val Gly Gly Phe Gly Ser		
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Tyr Gly Tyr Ser Ser Phe Asn Asn Arg Ala Asn Ser Leu Asn Ser Gly		
	1075 1080	1085
Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser Arg Ile Phe Ala Asn Gln		
	1090 1095	1100
His Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser		
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Ser Leu Asn Phe Lys Ser Ala Leu Leu Gln Asp Leu Asn Gln Ser Tyr		
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His Tyr Leu Ala Tyr Ser Ala Ala Thr Arg Ala Ser Tyr Gly Tyr Asp		
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Phe Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val  
 1155 1160 1165

Ser Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Thr Asn  
 1170 1175 1180

Gln Val Ala Leu Lys Asn Gly Ser Ser Ser Gln His Leu Phe Asn Ala  
 1185 1190 1195 1200

Ser Ala Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe  
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Tyr Met Asn Ala Gly Val Leu Gln Glu Phe Ala His Val Gly Ser Asn  
 1220 1225 1230

Asn Ala Ala Ser Leu Asn Thr Phe Lys Val Asn Ala Ala Arg Asn Pro  
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Leu Asn Thr His Ala Arg Val Met Met Gly Gly Glu Leu Lys Leu Ala  
 1250 1255 1260

Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile  
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<211> 5925

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
 Sequence

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<211> 1147

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Sequence

<400> 5

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Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Leu Lys Val  
20 25 30

Asp Asn Ala Val Ala Ser Tyr Asp Pro Asp Gln Lys Pro Ile Val Asp  
35 40 45

Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Gly Ile Ser Gln Leu  
50 55 60

Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn  
65 70 75 80

Gln Tyr Phe Ser Asp Phe Ile Asn Lys Ser Asn Asp Leu Ile Asn Lys  
85 90 95

Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys Ser Phe Gln Lys Phe  
100 105 110

Gly Asp Gln Arg Tyr Arg Ile Phe Thr Ser Trp Val Ser His Gln Asn  
115 120 125

Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg Asn Phe Met Glu Asn  
130 135 140

Ile Ile Gln Pro Pro Ile Leu Asp Asp Lys Glu Lys Ala Glu Phe Leu  
145 150 155 160

Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile  
165 170 175

Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu  
180 185 190

Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Thr Gly Gly Asp Trp Leu  
195 200 205

Asp Ile Phe Leu Ser Phe Ile Phe Asp Lys Lys Gln Ser Ser Asp Val  
 210 215 220

Lys Glu Ala Ile Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Ile  
 225 230 235 240

Ala Thr Thr Thr Thr Asp Ile Gln Gly Leu Pro Pro Glu Ala Arg Asp  
 245 250 255

Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met  
 260 265 270

Glu Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys  
 275 280 285

Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met  
 290 295 300

Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly  
 305 310 315 320

Gly Asn Gly Gly Pro Gly Ala Arg His Asp Trp Asn Ala Thr Val Gly  
 325 330 335

Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr Ile Ile Asn Val His  
 340 345 350

Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile  
 355 360 365

Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser  
 370 375 380

Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys Ile Asp Phe Met  
 385 390 395 400

Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Glu Lys  
 405 410 415

Glu Lys Glu Lys Phe Arg Thr Glu Ile Lys Asp Phe Gln Lys Asp Ser  
 420 425 430

Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg Ile Ala Phe Val Ser  
 435 440 445

Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr Glu Phe Gly Asn Gly  
 450 455 460

Asp Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala  
 465 470 475 480

Leu Asp Arg Glu Lys Asn Val Thr Leu Gln Gly Ser Leu Lys His Asp  
 485 490 495

Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser  
 500 505 510

Lys Asn Pro Asn Lys Gly Val Gly Val Thr Asn Gly Val Ser His Leu  
 515 520 525

Glu Val Gly Phe Asn Lys Val Ala Ile Phe Asn Leu Pro Asp Leu Asn  
 530 535 540

Asn Leu Ala Ile Thr Ser Phe Val Arg Arg Asn Leu Glu Asp Lys Leu  
 545 550 555 560

Thr Thr Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Ile Lys Asp  
 565 570 575

Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Thr Leu Asn Phe Asn  
 580 585 590

Lys Ala Val Ala Asp Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys  
 595 600 605

Lys Ala Gln Lys Asp Leu Glu Lys Ser Leu Arg Lys Arg Glu His Leu  
 610 615 620

Glu Lys Glu Val Glu Lys Lys Leu Glu Ser Lys Ser Gly Asn Lys Asn  
 625 630 635 640

Lys Met Glu Ala Lys Ala Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe  
 645 650 655

Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr  
 660 665 670

Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu  
 675 680 685

Asn Val Asn Lys Asn Leu Lys Asp Phe Asp Lys Ser Phe Asp Glu Phe  
 690 695 700

Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys  
 705 710 715 720

Ala	Leu	Lys	Gly	Ser	Val	Lys	Asp	Leu	Gly	Ile	Asn	Pro	Glu	Trp	Ile	725	730	735	
Ser	Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly	740	745	750	
Lys	Asn	Lys	Asp	Phe	Ser	Lys	Val	Thr	Gln	Ala	Lys	Ser	Asp	Leu	Glu	755	760	765	
Asn	Ser	Val	Lys	Asp	Val	Ile	Ile	Asn	Gln	Lys	Val	Thr	Asp	Lys	Val	770	775	780	
Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe	785	790	795	800
Ser	Arg	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu	805	810	815	
Gln	Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Ser	Leu	Asn	Ala	Arg	Lys	820	825	830	
Lys	Ser	Glu	Ile	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu	835	840	845	
Val	Gly	Asn	Gly	Leu	Ser	Gln	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn	850	855	860	
Phe	Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn	865	870	875	880
Asn	Asn	Asn	Asn	Asn	Gly	Leu	Lys	Asn	Glu	Pro	Ile	Tyr	Ala	Lys	Val	885	890	895	
Asn	Lys	Lys	Lys	Ala	Gly	Gln	Ala	Ala	Ser	Leu	Glu	Glu	Pro	Ile	Tyr	900	905	910	
Ala	Gln	Val	Ala	Lys	Lys	Val	Asn	Ala	Lys	Ile	Asp	Arg	Leu	Asn	Gln	915	920	925	
Ile	Ala	Ser	Gly	Leu	Gly	Val	Val	Gly	Gln	Ala	Ala	Gly	Phe	Pro	Leu	930	935	940	
Lys	Arg	His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Arg	945	950	955	960
Asn	Gln	Glu	Leu	Ala	Gln	Lys	Ile	Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser	965	970	975	

Glu Ala Lys Ala Gly Phe Phe Gly Asn Leu Glu Gln Thr Ile Asp Lys  
980 985 990

Leu Lys Asp Ser Thr Lys His Asn Pro Met Asn Leu Trp Val Glu Ser  
995 1000 1005

Ala Lys Lys Val Pro Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala  
1010 1015 1020

Thr Asn Ser His Ile Arg Ile Asn Ser Asn Ile Lys Asn Gly Ala Ile  
1025 1030 1035 1040

Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Pro Glu Trp Leu  
1045 1050 1055

Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Pro  
1060 1065 1070

Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp  
1075 1080 1085

Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys Leu Asn Asn Ala Val Lys  
1090 1095 1100

Asp Thr Asn Ser Gly Phe Thr Gln Phe Leu Thr Asn Ala Phe Ser Thr  
1105 1110 1115 1120

Ala Ser Tyr Tyr Cys Leu Ala Arg Glu Asn Ala Glu His Gly Ile Lys  
1125 1130 1135

Asn Val Asn Thr Lys Gly Gly Phe Gln Lys Ser  
1140 1145

<210> 6

<211> 546

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Sequence

<400> 6

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe  
1 5 10 15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro

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Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile		
35	40	45
Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro		
50	55	60
Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr		
65	70	75
Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr		
85	90	95
Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro		
100	105	110
Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn		
115	120	125
Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr		
130	135	140
Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu		
145	150	155
Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val		
165	170	175
Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met		
180	185	190
Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu		
195	200	205
Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys		
210	215	220
Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met		
225	230	235
Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu		
245	250	255
Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile		
260	265	270
Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu		



275	280	285
Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu		
290	295	300
Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly		
305	310	315 320
Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly		
325	330	335
His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile		
340	345	350
Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu		
355	360	365
Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser		
370	375	380
Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser		
385	390	395 400
Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala		
405	410	415
Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp		
420	425	430
Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu		
435	440	445
Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn		
450	455	460
Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly		
465	470	475 480
Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val		
485	490	495
Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu		
500	505	510
Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Thr Pro		
515	520	525
Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly		

Met Met

545

&lt;210&gt; 7

&lt;211&gt; 1838

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificial  
Sequence

&lt;400&gt; 7

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<210> 8  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Sequence

<400> 8  
gactcgagtc gacatcga

18